

SEQUENCE LISTING

<110> NeuroSearch A/S

<120> Novel potassium channels and genes encoding these potassium channels.

<130> 128-200-US

<140>

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<160> 32

<170> PatentIn Ver. 2.1

<210> 1

<211> 2335

<212> DNA

<213> Homo sapiens

<220>

<221> gene

<222> (1)..(2335)

<220>

<221> CDS

<222> (83)..(2170)

<223> KCNQ4

<400> 1

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cgccccccagc cgggcgcgcg cc atg gcc gag gcc ccc ccg cgc cgc ctc ggc 112
                               Met Ala Glu Ala Pro Pro Arg Arg Leu Gly
                               1                               5                               10

ctg ggt ccc ccg ccc ggg gac gcc ccc cgc gcg gag cta gtg gcg ctc 160
Leu Gly Pro Pro Pro Gly Asp Ala Pro Arg Ala Glu Leu Val Ala Leu
                               15                               20                               25

acg gcc gtg cag agc gaa cag ggc gag gcg ggc ggg ggc ggc tcc ccg 208
Thr Ala Val Gln Ser Glu Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro
                               30                               35                               40

cgc cgc ctc ggc ctc ctg ggc agc ccc ctg ccg ccg ggc gcg ccc ctc 256
Arg Arg Leu Gly Leu Leu Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu
                               45                               50                               55

cct ggg ccg ggc tcc ggc tcg ggc tcc gcc tgc ggc cag cgc tcc tcg 304
Pro Gly Pro Gly Ser Gly Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser
                               60                               65                               70

gcc gcg cac aag cgc tac cgc cgc ctg cag aac tgg gtc tac aac gtg 352
Ala Ala His Lys Arg Tyr Arg Arg Leu Gln Asn Trp Val Tyr Asn Val
                               75                               80                               85

ctg gag cgg ccc cgc ggc tgg gcc ttc gtc tac cac gtc ttc ata ttt 400
Leu Glu Arg Pro Arg Gly Trp Ala Phe Val Tyr His Val Phe Ile Phe
                               95                               100                               105

ttg ctg gtc ttc agc tgc ctg gtg ctg tct gtg ctg tcc act atc cag 448
Leu Leu Val Phe Ser Cys Leu Val Leu Ser Val Leu Ser Thr Ile Gln
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gag cac cag gaa ctt gcc aac gag tgt ctc ctc atc ttg gaa ttc gtg Glu His Gln Glu Leu Ala Asn Glu Cys Leu Leu Ile Leu Glu Phe Val 125 130 135	496
atg atc gtg gtt ttc ggc ttg gag tac atc gtc cgg gtc tgg tcc gcc Met Ile Val Val Phe Gly Leu Glu Tyr Ile Val Arg Val Trp Ser Ala 140 145 150	544
gga tgc tgc tgc cgc tac cga gga tgg cag ggt cgc ttc cgc ttt gcc Gly Cys Cys Cys Arg Tyr Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala 155 160 165 170	592
aga aag ccc ttc tgt gtc atc gac ttc atc gtg ttc gtg gcc tcg gtg Arg Lys Pro Phe Cys Val Ile Asp Phe Ile Val Phe Val Ala Ser Val 175 180 185	640
gcc gtc atc gcc gcg ggt acc cag ggc aac atc ttc gcc acg tcc gcg Ala Val Ile Ala Ala Gly Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala 190 195 200	688
ctg cgc agc atg cgc ttc ctg cag atc ctg cgc atg gtg cgc atg gac Leu Arg Ser Met Arg Phe Leu Gln Ile Leu Arg Met Val Arg Met Asp 205 210 215	736
cgc cgc ggc ggc acc tgg aag ctg ctg ggc tca gtg gtc tac gcg cat Arg Arg Gly Gly Thr Trp Lys Leu Leu Gly Ser Val Val Tyr Ala His 220 225 230	784
agc aag gag ctg atc acc gcc tgg tac atc ggg ttc ctg gtg ctc atc Ser Lys Glu Leu Ile Thr Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile 235 240 245 250	832
ttc gcc tcc ttc ctg gtc tac ctg gcc gag aag gac gcc aac tcc gac Phe Ala Ser Phe Leu Val Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp 255 260 265	880
ttc tcc tcc tac gcc gac tcg ctc tgg tgg ggg acg att aca ttg aca Phe Ser Ser Tyr Ala Asp Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr 270 275 280	928
acc atc ggc tat ggt gac aag aca ccg cac aca tgg ctg ggc agg gtc Thr Ile Gly Tyr Gly Asp Lys Thr Pro His Thr Trp Leu Gly Arg Val 285 290 295	976
ctg gct gct ggc ttc gcc tta ctg ggc atc tct ttc ttt gcc ctg cct Leu Ala Ala Gly Phe Ala Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro 300 305 310	1024
gcc ggc atc cta ggc tcc ggc ttt gcc ctg aag gtc cag gag cag cac Ala Gly Ile Leu Gly Ser Gly Phe Ala Leu Lys Val Gln Glu Gln His 315 320 325 330	1072
cgg cag aag cac ttc gag aag cgg agg atg ccg gca gcc aac ctc atc Arg Gln Lys His Phe Glu Lys Arg Arg Met Pro Ala Ala Asn Leu Ile 335 340 345	1120
cag gct gcc tgg cgc ctg tac tcc acc gat atg agc cgg gcc tac ctg Gln Ala Ala Trp Arg Leu Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu 350 355 360	1168
aca gcc acc tgg tac tac tat gac agt atc ctc cca tcc ttc aga gag Thr Ala Thr Trp Tyr Tyr Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu 365 370 375	1216

ctg gcc ctc ttg ttt gag cac gtg caa cgg gcc cgc aat ggg ggc cta Leu Ala Leu Leu Phe Glu His Val Gln Arg Ala Arg Asn Gly Gly Leu 380 385 390	1264
cgg ccc ctg gag gtg cgg cgg gcg ccg gta ccc gac gga gca ccc tcc Arg Pro Leu Glu Val Arg Arg Ala Pro Val Pro Asp Gly Ala Pro Ser 395 400 405 410	1312
cgt tac ccg ccc gtt gcc acc tgc cac cgg ccg ggc agc acc tcc ttc Arg Tyr Pro Pro Val Ala Thr Cys His Arg Pro Gly Ser Thr Ser Phe 415 420 425	1360
tgc cct ggg gaa agc agc cgg atg ggc atc aaa gac cgc atc cgc atg Cys Pro Gly Glu Ser Ser Arg Met Gly Ile Lys Asp Arg Ile Arg Met 430 435 440	1408
ggc agc tcc cag cgg cgg acg ggt cct tcc aag cag cag ctg gca cct Gly Ser Ser Gln Arg Arg Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro 445 450 455	1456
cca aca atg ccc acc tcc cca agc agc gag cag gtg ggt gag gcc acc Pro Thr Met Pro Thr Ser Pro Ser Ser Glu Gln Val Gly Glu Ala Thr 460 465 470	1504
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ttc cgg gca tct ctg aga ctc aaa ccc cgc acc tct gct gag gat gcc Phe Arg Ala Ser Leu Arg Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala 495 500 505	1600
ccc tca gag gaa gta gca gag gag aag agc tac cag tgt gag ctc acg Pro Ser Glu Glu Val Ala Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr 510 515 520	1648
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att ctc aag ttc ctg gtg gcc aaa agg aaa ttc aag gag aca ctg cga Ile Leu Lys Phe Leu Val Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg 540 545 550	1744
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gtg ggt cgg ggg ccc ggg gac agg aag gcc cgg gag aag ggc gac aag Val Gly Arg Gly Pro Gly Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys 590 595 600	1888
ggg ccc tcc gac gcg gag gtg gtg gat gaa atc agc atg atg gga cgc Gly Pro Ser Asp Ala Glu Val Val Asp Glu Ile Ser Met Met Gly Arg 605 610 615	1936
gtg gtc aag gtg gag aag cag gtg cag tcc atc gag cac aag ctg gac Val Val Lys Val Glu Lys Gln Val Gln Ser Ile Glu His Lys Leu Asp 620 625 630	1984

ctg ctg ttg ggc ttc tat tgc cgc tgc ctg cgc tct ggc acc tgc gcc 2032
 Leu Leu Leu Gly Phe Tyr Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala
 635 640 645 650
 agc ctg ggc gcc gtg caa gtg ccg ctg ttc gac ccc gac atc acc tcc 2080
 Ser Leu Gly Ala Val Gln Val Pro Leu Phe Asp Pro Asp Ile Thr Ser
 655 660 665
 gac tac cac agc cct gtg gac cac gag gac atc tcc gtc tcc gca cag 2128
 Asp Tyr His Ser Pro Val Asp His Glu Asp Ile Ser Val Ser Ala Gln
 670 675 680
 acg ctc agc atc tcc cgc tgc gtc agc acc aac atg gac tga 2170
 Thr Leu Ser Ile Ser Arg Ser Val Ser Thr Asn Met Asp
 685 690 695
 gggacttctc agaggcaggg cagcacacgg ccagccccgc ggcttgggcg tccgactgcc 2230
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 Gln Gly Glu Ala Gly Gly Gly Gly Ser Pro Arg Arg Leu Gly Leu Leu
 35 40 45
 Gly Ser Pro Leu Pro Pro Gly Ala Pro Leu Pro Gly Pro Gly Ser Gly
 50 55 60
 Ser Gly Ser Ala Cys Gly Gln Arg Ser Ser Ala Ala His Lys Arg Tyr
 65 70 75 80
 Arg Arg Leu Gln Asn Trp Val Tyr Asn Val Leu Glu Arg Pro Arg Gly
 85 90 95
 Trp Ala Phe Val Tyr His Val Phe Ile Phe Leu Leu Val Phe Ser Cys
 100 105 110
 Leu Val Leu Ser Val Leu Ser Thr Ile Gln Glu His Gln Glu Leu Ala
 115 120 125
 Asn Glu Cys Leu Leu Ile Leu Glu Phe Val Met Ile Val Val Phe Gly
 130 135 140
 Leu Glu Tyr Ile Val Arg Val Trp Ser Ala Gly Cys Cys Cys Arg Tyr
 145 150 155 160
 Arg Gly Trp Gln Gly Arg Phe Arg Phe Ala Arg Lys Pro Phe Cys Val
 165 170 175
 Ile Asp Phe Ile Val Phe Val Ala Ser Val Ala Val Ile Ala Ala Gly
 180 185 190

Thr Gln Gly Asn Ile Phe Ala Thr Ser Ala Leu Arg Ser Met Arg Phe
 195 200 205
 Leu Gln Ile Leu Arg Met Val Arg Met Asp Arg Arg Gly Gly Thr Trp
 210 215 220
 Lys Leu Leu Gly Ser Val Val Tyr Ala His Ser Lys Glu Leu Ile Thr
 225 230 235 240
 Ala Trp Tyr Ile Gly Phe Leu Val Leu Ile Phe Ala Ser Phe Leu Val
 245 250 255
 Tyr Leu Ala Glu Lys Asp Ala Asn Ser Asp Phe Ser Ser Tyr Ala Asp
 260 265 270
 Ser Leu Trp Trp Gly Thr Ile Thr Leu Thr Thr Ile Gly Tyr Gly Asp
 275 280 285
 Lys Thr Pro His Thr Trp Leu Gly Arg Val Leu Ala Ala Gly Phe Ala
 290 295 300
 Leu Leu Gly Ile Ser Phe Phe Ala Leu Pro Ala Gly Ile Leu Gly Ser
 305 310 315 320
 Gly Phe Ala Leu Lys Val Gln Glu Gln His Arg Gln Lys His Phe Glu
 325 330 335
 Lys Arg Arg Met Pro Ala Ala Asn Leu Ile Gln Ala Ala Trp Arg Leu
 340 345 350
 Tyr Ser Thr Asp Met Ser Arg Ala Tyr Leu Thr Ala Thr Trp Tyr Tyr
 355 360 365
 Tyr Asp Ser Ile Leu Pro Ser Phe Arg Glu Leu Ala Leu Leu Phe Glu
 370 375 380
 His Val Gln Arg Ala Arg Asn Gly Gly Leu Arg Pro Leu Glu Val Arg
 385 390 395 400
 Arg Ala Pro Val Pro Asp Gly Ala Pro Ser Arg Tyr Pro Pro Val Ala
 405 410 415
 Thr Cys His Arg Pro Gly Ser Thr Ser Phe Cys Pro Gly Glu Ser Ser
 420 425 430
 Arg Met Gly Ile Lys Asp Arg Ile Arg Met Gly Ser Ser Gln Arg Arg
 435 440 445
 Thr Gly Pro Ser Lys Gln Gln Leu Ala Pro Pro Thr Met Pro Thr Ser
 450 455 460
 Pro Ser Ser Glu Gln Val Gly Glu Ala Thr Ser Pro Thr Lys Val Gln
 465 470 475 480
 Lys Ser Trp Ser Phe Asn Asp Arg Thr Arg Phe Arg Ala Ser Leu Arg
 485 490 495
 Leu Lys Pro Arg Thr Ser Ala Glu Asp Ala Pro Ser Glu Glu Val Ala
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 Glu Glu Lys Ser Tyr Gln Cys Glu Leu Thr Val Asp Asp Ile Met Pro
 515 520 525
 Ala Val Lys Thr Val Ile Arg Ser Ile Arg Ile Leu Lys Phe Leu Val
 530 535 540

6

Ala Lys Arg Lys Phe Lys Glu Thr Leu Arg Pro Tyr Asp Val Lys Asp
 545 550 555 560

Val Ile Glu Gln Tyr Ser Ala Gly His Leu Asp Met Leu Gly Arg Ile
 565 570 575

Lys Ser Leu Gln Thr Arg Val Asp Gln Ile Val Gly Arg Gly Pro Gly
 580 585 590

Asp Arg Lys Ala Arg Glu Lys Gly Asp Lys Gly Pro Ser Asp Ala Glu
 595 600 605

Val Val Asp Glu Ile Ser Met Met Gly Arg Val Val Lys Val Glu Lys
 610 615 620

Gln Val Gln Ser Ile Glu His Lys Leu Asp Leu Leu Leu Gly Phe Tyr
 625 630 635 640

Ser Arg Cys Leu Arg Ser Gly Thr Ser Ala Ser Leu Gly Ala Val Gln
 645 650 655

Val Pro Leu Phe Asp Pro Asp Ile Thr Ser Asp Tyr His Ser Pro Val
 660 665 670

Asp His Glu Asp Ile Ser Val Ser Ala Gln Thr Leu Ser Ile Ser Arg
 675 680 685

Ser Val Ser Thr Asn Met Asp
 690 695

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 <213> Artificial Sequence

<220>
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<210> 4
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 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 4
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<210> 5
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<220>
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<210> 10
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<220>
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<210> 16
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<220>
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<400> 21
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<210> 22
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<210> 23
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<210> 24
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<400> 24
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<210> 26
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<210> 28
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<400> 18
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<210> 29
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<220>
<223> Description of Artificial Sequence: PCR primer

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<210> 31
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